

Roland Arnold

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

5,618
citations

159573

30
h-index

197805

49
g-index

56
all docs

56
docs citations

56
times ranked

13109
citing authors

#	ARTICLE	IF	CITATIONS
1	COVID-19 mortality in patients with cancer on chemotherapy or other anticancer treatments: a prospective cohort study. <i>Lancet, The</i> , 2020, 395, 1919-1926.	13.7	908
2	Gepard: a rapid and sensitive tool for creating dotplots on genome scale. <i>Bioinformatics</i> , 2007, 23, 1026-1028.	4.1	639
3	eggNOG v3.0: orthologous groups covering 1133 organisms at 41 different taxonomic ranges. <i>Nucleic Acids Research</i> , 2012, 40, D284-D289.	14.5	490
4	COVID-19 prevalence and mortality in patients with cancer and the effect of primary tumour subtype and patient demographics: a prospective cohort study. <i>Lancet Oncology, The</i> , 2020, 21, 1309-1316.	10.7	473
5	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermuted cancers. <i>Nature Genetics</i> , 2015, 47, 257-262.	21.4	306
6	Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376.	4.7	230
7	The binary protein-protein interaction landscape of <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2014, 32, 285-290.	17.5	218
8	EffectiveDB updates and novel features for a better annotation of bacterial secreted proteins and Type III, IV, VI secretion systems. <i>Nucleic Acids Research</i> , 2016, 44, D669-D674.	14.5	172
9	probeCheck – a central resource for evaluating oligonucleotide probe coverage and specificity. <i>Environmental Microbiology</i> , 2008, 10, 2894-2898.	3.8	170
10	MIPS Arabidopsisthaliana Database (MATDB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93.	14.5	159
11	A Transcriptionally Distinct CXCL13+CD103+CD8+ T-cell Population Is Associated with B-cell Recruitment and Neoantigen Load in Human Cancer. <i>Cancer Immunology Research</i> , 2019, 7, 784-796.	3.4	141
12	The Genome of the Amoeba Symbiont <i>Candidatus</i> <i>Amoebophilus asiaticus</i> Reveals Common Mechanisms for Host Cell Interaction among Amoeba-Associated Bacteria. <i>Journal of Bacteriology</i> , 2010, 192, 1045-1057.	2.2	138
13	B2G-FAR, a species-centered GO annotation repository. <i>Bioinformatics</i> , 2011, 27, 919-924.	4.1	137
14	Large-scale interaction profiling of PDZ domains through proteomic peptide-phage display using human and viral phage peptidomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2542-2547.	7.1	124
15	Effective–a database of predicted secreted bacterial proteins. <i>Nucleic Acids Research</i> , 2011, 39, D591-D595.	14.5	102
16	The evolutionary landscape of colorectal tumorigenesis. <i>Nature Ecology and Evolution</i> , 2018, 2, 1661-1672.	7.8	99
17	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	14.5	97
18	Quantitative Genome-Wide Genetic Interaction Screens Reveal Global Epistatic Relationships of Protein Complexes in <i>Escherichia coli</i> . <i>PLoS Genetics</i> , 2014, 10, e1004120.	3.5	96

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19	Genetic Interaction Maps in <i>Escherichia coli</i> Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways. <i>PLoS Genetics</i> , 2011, 7, e1002377.	3.5	95
20	A negative genetic interaction map in isogenic cancer cell lines reveals cancer cell vulnerabilities. <i>Molecular Systems Biology</i> , 2013, 9, 696.	7.2	90
21	Severity of COVID-19 in children with cancer: Report from the United Kingdom Paediatric Coronavirus Cancer Monitoring Project. <i>British Journal of Cancer</i> , 2021, 124, 754-759.	6.4	72
22	Molecular recognition determinants for type IV secretion of diverse families of conjugative relaxases. <i>Molecular Microbiology</i> , 2010, 78, 1539-1555.	2.5	57
23	The UK Coronavirus Cancer Monitoring Project: protecting patients with cancer in the era of COVID-19. <i>Lancet Oncology</i> , 2020, 21, 622-624.	10.7	53
24	Computational analysis of interactomes: Current and future perspectives for bioinformatics approaches to model the host-pathogen interaction space. <i>Methods</i> , 2012, 57, 508-518.	3.8	49
25	Proteome-wide analysis of phospho-regulated PDZ domain interactions. <i>Molecular Systems Biology</i> , 2018, 14, e8129.	7.2	48
26	SIMAP: the similarity matrix of proteins. <i>Nucleic Acids Research</i> , 2006, 34, D252-D256.	14.5	44
27	SIMAP—a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , 2010, 38, D223-D226.	14.5	40
28	Novel function discovery with GeneMANIA: a new integrated resource for gene function prediction in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2015, 31, 306-310.	4.1	38
29	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016, 16, 2032-2046.	6.4	36
30	SIMAP—The similarity matrix of proteins. <i>Bioinformatics</i> , 2005, 21, ii42-ii46.	4.1	35
31	Mortality Among Adults With Cancer Undergoing Chemotherapy or Immunotherapy and Infected With COVID-19. <i>JAMA Network Open</i> , 2022, 5, e220130.	5.9	34
32	SIMAP structuring the network of protein similarities. <i>Nucleic Acids Research</i> , 2007, 36, D289-D292.	14.5	24
33	SIMAP—the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , 2014, 42, D279-D284.	14.5	24
34	Proteomic peptide phage display uncovers novel interactions of the PDZ1 supramodule of syntenin. <i>FEBS Letters</i> , 2016, 590, 3-12.	2.8	24
35	Targeting effectors: the molecular recognition of Type III secreted proteins. <i>Microbes and Infection</i> , 2010, 12, 346-358.	1.9	23
36	Key findings from the UKCCMP cohort of 877 patients with haematological malignancy and COVID-19: disease control as an important factor relative to recent chemotherapy or anti-CD20 therapy. <i>British Journal of Haematology</i> , 2022, 196, 892-901.	2.5	23

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37	Srrm234, but not canonical SR and hnRNP proteins, drive inclusion of <i>Dscam</i> exon 9 variable exons. <i>Rna</i> , 2019, 25, 1353-1365.	3.5	16
38	COVID-19 in children with haematological malignancies. <i>Archives of Disease in Childhood</i> , 2022, 107, 186-188.	1.9	14
39	Dynamically expressed single ELAV/Hu orthologue <i>elavl2</i> of bees is required for learning and memory. <i>Communications Biology</i> , 2021, 4, 1234.	4.4	12
40	In situ functional dissection of RNA cis-regulatory elements by multiplex CRISPR-Cas9 genome engineering. <i>Nature Communications</i> , 2017, 8, 2109.	12.8	11
41	Back-Splicing Transcript Isoforms (Circular RNAs) Affect Biologically Relevant Pathways and Offer an Additional Layer of Information to Stratify NMIBC Patients. <i>Frontiers in Oncology</i> , 2020, 10, 812.	2.8	11
42	Non-Coding Mutations in Urothelial Bladder Cancer: Biological and Clinical Relevance and Potential Utility as Biomarkers. <i>Bladder Cancer</i> , 2019, 5, 263-272.	0.4	10
43	Tropomyosins: Potential Biomarkers for Urothelial Bladder Cancer. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1102.	4.1	7
44	Trends in urine biomarker discovery for urothelial bladder cancer: DNA, RNA, or protein?. <i>Translational Andrology and Urology</i> , 2021, 10, 2787-2808.	1.4	7
45	Functional analysis of the <i>finO</i> distal region of plasmid R1. <i>Plasmid</i> , 2011, 65, 159-168.	1.4	6
46	Molecular Subtypes of T1 Bladder Cancer: Biomolecular Characteristics Versus Clinical Utility. <i>European Urology</i> , 2020, 78, 538-539.	1.9	4
47	Urine DNA for monitoring chemoradiotherapy response in muscle-invasive bladder cancer: a pilot study. <i>BJU International</i> , 2021, , .	2.5	3
48	STAG2 Protein Expression in Non-muscle-invasive Bladder Cancer: Associations with Sex, Genomic and Transcriptomic Changes, and Clinical Outcomes. <i>European Urology Open Science</i> , 2022, 38, 88-95.	0.4	3
49	Establishing the Bladder Cancer Research Centre at the University of Birmingham. <i>Nature Reviews Urology</i> , 2021, 18, 318-320.	3.8	1
50	PAT: predictor for structured units and its application for the optimization of target molecules for the generation of synthetic antibodies. <i>BMC Bioinformatics</i> , 2016, 17, 150.	2.6	0
51	Abstract B09: DNA polymerase mutations trigger rapid onset of ultra-hypermutant malignant brain tumors in children with biallelic mismatch repair deficiency. , 2015, , .		0
52	Metastatic disease representation: An analysis of 148 paired colorectal cancer lymph node metastatic tumour deposits.. <i>Journal of Clinical Oncology</i> , 2018, 36, e15595-e15595.	1.6	0